

FIGURE 1

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1 ACATAGCTTT TATGTGAAGG AAAAATCAAA TTTCCAAA TTTGGAGTTT
51 ATAGACTGAG CACATGATAC TGTCGGTGTT TGTTAAAAG ATTAAAAAC
101 TATACCCTTT GAATAATTAA ATTAAATCAA ATTTTCATAT TAAATTTT
151 ATTTTATAGT AATAATCTAA TTTAATACA CTTAGGTGTA AAAAAAATT
201 AAGCTTCAAA GTTTTATATT GTCAGCAAT CACAATAAT TGTGTGTACG
251 GATACAAAGT CAAACATGAT TTATTGACGG TGTAAAAAT CTTTACAGTG
301 ACAATGTATA TGGATTAAAT CGATTTTATA TTAGTTATTT TATGTTATAT
351 CGTATTCATG TCATGTGTTT TGTACTGATC TTGTGTCATA GTTCAAACA
401 CTGATAGTTT AACTGAAGG CGGGAAACGA CAATCTGATC CCCATCAAGC
451 TTCTGCAGGT CCTGCTCGAG TGGAAGCTAA TTCTCAGTCC AAAGCCTCAA
501 CAAGGTCAGG GTACAGAGTC TCCAAACCAT TAGCCAAAAG CTACAGGAGA
551 TCAATGAAGA ATCTTCAATC AAAGTAACT ACTGTCCAG CACATGCATC
601 ATGGTCAGTA AGTTTCAGAA AAAGACATCC ACCGAAGACT TAAAGTTAGT
651 GGGCATCTTT GAAAGTAATC TTGTCAAC

FIGURE 2

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1 GAACTTTCCT TTATGTAATT TTCCAGAATC CTTGTCAGAT TCTAATCATT
51 'GCTTTATAAT TATAGTTATA CTCATGGATT TGTAGTTGAG TATGAAAATA
101 TTTTSTAATG CATTTTATGA CTTGCCAATT GATTGACAAC ATGCATCAAT
151 CGACCTGCAG CCACTCGAAG CGGCCGCCAC TCGAGTGGTG GCCGCATCGA
201 TCGTGAAGTT TCTCATCTAA GCCCCCATTI GGACGTGAAT GTAGACACGT
251 CGAAATAAAG ATTTCCGAAT TAGAATAATT TGTTTATTGC TTTGCGCTAT
301 AAATACGACG GATCGTATGC ATTAAATATA TAGAGGAATT TCTTATCTTG
351 CTAATTCAG CATAGTTATT TTAATTGTC AAATAATTGT ATGAATGGTA
401 TATTCTACAA CTTTCTCATG CTTTCAATA ATGATGTTGT TTTTCTGTAA
451 TGCTATTTTG ATTTTATTTT GCAGGTGAAC AAGAGCAACA GTGCTTTGAT
501 CCATATTACA AATGAGGGAT GGTACTATTT TATGGATGCA GTGAACTTC
551 TGAAAACATA GTTGGTGTGS TGCTGTTGGA G

FIGURE 3

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1 TTTCTTACTT CCTAGATTG GTAGGGTTGA AACACATGAA AATTTAAAGC
51 ATATACACAA TACATTTTGG ACTTGACTTG ACTTCACTAT TCATAATGAG
101 CTTCATGCAT ATTTGGATGC CCATATCATA TCAAGTCATT ATTTATTTT
151 CCTTTTAACG ATTACCCCTT CCTACTTTT TCCTTCTTG CCGGGACAAG
201 GTCATCCAAA CTGAAGTGTT CGGTGGGAAA CGACACTCTG ATCCCCATCA
251 AGCTTCTGCA GGTCCCTGCTC GAGTGGAAGC TAATTCTCAG TCCAAAGCCT
301 CAACAAGGTC AGGGTACAGA GTCTCCAAAC CATTAGCCAA AAGCTACAGG
351 AGATCAATGA AGAATCTTCA ATCAAAGTAA ACTACTGTTC CAGCACATGC
401 ATCATGGTCA GTAAGTTTCA GAAAAAGACA TCCACCGAAG ACTTAAAGTT
451 AGTGGGCATC TTGAAAAGTA ATCTTGTCAA C

FIGURE 4

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1 GAACCTTCCT TTATGTAATT TTCCAGAATC CTTGTCAGAT TCTAATCATT
51 GCTTTATAAT TATAGTTATA CTCATGGATT TGTAGTTGAG TATGAAAATA
101 TTTTTTAATG CATTTTATGA CTTGCCAATT GATTGACAAC ATGCATCAAT
151 CGACCTGCAG CCACTCGAAG CGGCCGCCAC TCGAGTGGTG GCCGCATCGA
201 TCGTGAAGTT TCTCATCTAA GCCCCCATTT GGACGTGAAT GTAGACACGT
251 CGAAATAAAG ATTTCCGAAT TAGAATAATT TGTTTATTGC TTTCGCCTAT
301 AAATACGACG GATCGTAATT TGTCGTTTTA TCAAAATGTA CTTTCATTTT
351 ATAATAACTT CCATTTTTTT TTTCTTTTTT TTTTATAATA ACAGAAAAAG
401 AAAAAGAAAG ATGATGAAAA GAGAAAAGAG AAAACCGAAC CATGATAATT
451 AACACACCAC GTGCAATTTA CTTTACTTTA ATTTTACTAC TACCTTATTC
501 TTTCTTCAGC GTGGTAACCG TTATACTCTT TATTACACCA CTCACCACCA

FIGURE 5

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A 5'ACATAGCTTTTATGTGAAGGAAAAATC 3' (SEQ ID NO:9)
E 5'TTTCTTACTTCCTAGATTTGGTAGG 3' (SEQ ID NO:10)
Z 5'GTTGACAAGATTACTTTCAAAGATGC 3' (SEQ ID NO:11)
B 5'CTCCAACAGCACCACACCAACTAT 3' (SEQ ID NO:12)
F 5'TGGTGGTGAGTGGTGTAAATAAGAG 3' (SEQ ID NO:13)
Y 5'GAAC TTCCTTTATGTAATTTTCCAG 3' (SEQ ID NO:14)

FIGURE 6

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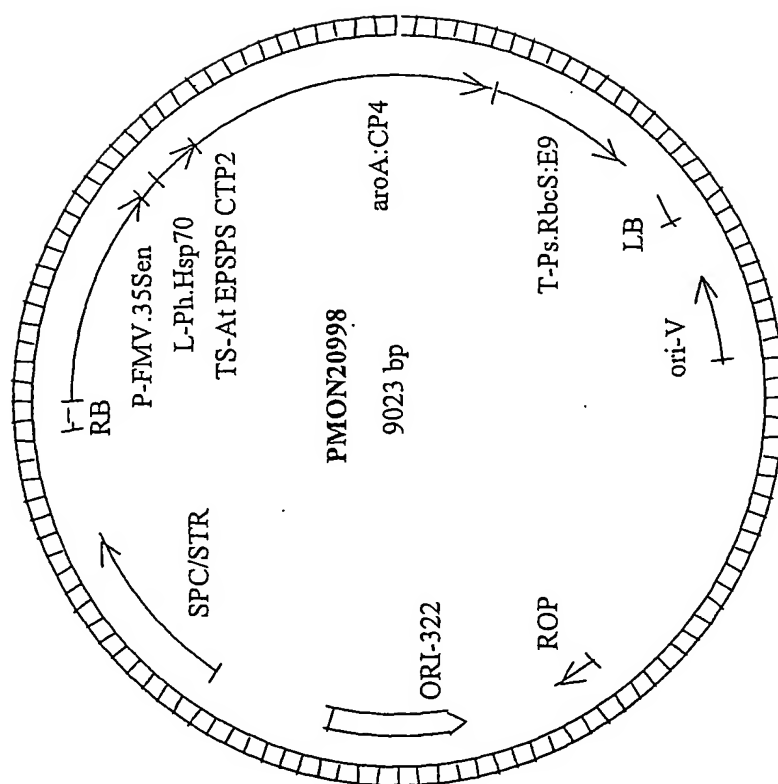


FIGURE 7